

STIC-ILL

Fr m: Ponnaluri, Padmashri  
Sent: Thursday, September 25, 2003 3:42 PM  
To: STIC-ILL  
Subject: A request for copy of reference:

Adon  
my  
32

Please send me a copy of the following reference:

- 1) Sche, Paul P.; McKenzie, Kathleen M.; White, Jennifer D.; Austin, David J.  
CS Department of Chemistry, Yale University, New Haven, CT, 06511, USA  
SO Chemistry & Biology (1999) 6(10) 707-716  
CODEN: CBOLE2; ISSN: 1074-5521.
- 2) Zuccon et al., Journal of Molecular Biology, vol. 307, issue 5, 13 April 2001, pages 1329-1339.
- 3) Analysis of bacteriophage T7 gene 10A and frameshifted 10B proteins.  
AU Siple J; Stassi D; Dunn J; Goldman E  
CS Department of Microbiology and Molecular Genetics, University of Medicine and Dentistry of New Jersey, Newark 07103.  
NC CA00890 (NCI)  
GM27711 (NIGMS)  
SO GENE EXPRESSION, (1991 May) 1 (2) 127-36.  
Journal code: 9200651. ISSN: 1052-2166.
- 4) Condreay J P; Wright S E; Molineux I J  
CS Department of Microbiology, University of Texas, Austin 78712.  
NC GM32095 (NIGMS)  
SO JOURNAL OF MOLECULAR BIOLOGY, (1989 Jun 5) 207 (3) 555-61.  
Journal code: 2985088R. ISSN: 0022-2836.  
CY ENGLAND: United Kingdom.
- 5) Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 genetic elements  
AU Dunn, John J.; Studier, F. William  
CS Biol. Dep., Brookhaven Natl. Lab., Upton, NY, 11973, USA  
SO Journal of Molecular Biology (1983), 166(4), 477-535  
CODEN: JMOBAK; ISSN: 0022-2836.

(file reference: 09/836,865)

thanks

PonnaluriShri

Patent Examiner

Art Unit 1639

Tech Center 1600

703-305-3884

CM1, 3D07.

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Q H301, J73

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CODEN: CBOLE2; ISSN: 1074-5521.

2) Zuccon et al., Journal of Molecular Biology, vol. 307, issue 5, 13 April 2001, pages 1329-1339.

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10/9/25  
465769

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1801358

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AU Siple J; Stassi D; Dunn J; Goldman E  
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(file reference: 09/836,865)

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Patent Examiner  
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Tech Center 1600  
703-305-3884  
CM1, 3D07.

(FILE 'HOME' ENTERED AT 15:18:12 ON 25 SEP 2003)

FILE 'MEDLINE, CAPLUS' ENTERED AT 15:18:27 ON 25 SEP 2003

L1 4460 S T7 (10A) BACTERIOPHAGE  
L2 3 S L1 AND PANNING

FILE 'STNGUIDE' ENTERED AT 15:20:59 ON 25 SEP 2003

FILE 'MEDLINE, CAPLUS' ENTERED AT 15:21:44 ON 25 SEP 2003

L3 0 S SCHE/AU  
E SCHE P P/AU  
L4 9 S E3-E4

FILE 'STNGUIDE' ENTERED AT 15:23:01 ON 25 SEP 2003

L5 0 S L1 AND (GENE (A) 10A)

FILE 'MEDLINE, CAPLUS' ENTERED AT 15:31:58 ON 25 SEP 2003

L6 3 S L1 AND (GENE (A) 10A)  
L7 1644 S SYNAPTOTAGMIN OR SYTIV  
L8 0 S L7 AND L1  
L9 10 S SYTI  
L10 6104 S L7 OR L1  
L11 176 S LIBRAR? AND L10  
L12 135 S L11 AND L1  
L13 1646 S L7 OR L9  
L14 0 S L13 AND L1  
L15 41 S L13 AND LIBRAR?  
L16 0 S L15 AND BACTERIOPHAGE  
L17 1 S L15 AND PHAGE  
L18 135 S L1 AND LIBRAR?  
L19 7 S L18 AND ARRAY#

FILE 'STNGUIDE' ENTERED AT 15:40:13 ON 25 SEP 2003

=> d 19 1-8

L9 ANSWER 1 OF 8 CAPLUS COPYRIGHT 2003 ACS on STN  
AN 2003:9270 CAPLUS  
DN 138:151776  
TI Automation of **phage** display for high-throughput antibody  
development  
AU Konthur, Zoltan; Walter, Gerald  
CS Max Planck Institute of Molecular Genetics, Berlin, DE-14195, Germany  
SO Targets (2002), 1(1), 30-36  
CODEN: TARGB9; ISSN: 1477-3627  
PB Elsevier Science Ltd.  
DT Journal; General Review  
LA English

RE.CNT 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 2 OF 8 CAPLUS COPYRIGHT 2003 ACS on STN  
AN 2002:466050 CAPLUS  
DN 137:46066  
TI Protein **arrays** comprising plural antibodies or fragments  
obtained from Camelidae for diagnosis  
IN De Haard, Johannes Joseph Wilhelmus; Hermans, Pim; Landa, Ilse; Verrips,  
Cornelis Theodorus  
PA Unilever N.V., Neth.; Unilever PLC; Hindustan Lever Ltd.  
SO PCT Int. Appl., 80 pp.  
CODEN: PIXXD2  
DT Patent  
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002048193	A2	20020620	WO 2001-EP14471	20011203
	WO 2002048193	A3	20030814		
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
	AU 2002029639	A5	20020624	AU 2002-29639	20011203
PRAI	EP 2000-311142	A	20001213		
	WO 2001-EP14471	W	20011203		

L9 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2003 ACS on STN  
AN 2002:172157 CAPLUS  
DN 136:227895  
TI Compositions and methods for the generation of single stranded cDNA  
microarrays with accurate universal quantitation reference  
IN Zhang, Wei; Hu, Limei; Hamilton, Stanley R.  
PA Board of Regents, the University of Texas System, USA  
SO PCT Int. Appl., 48 pp.  
CODEN: PIXXD2  
DT Patent  
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI WO 2002018655 A2 20020307 WO 2001-US27021 20010830  
 WO 2002018655 A3 20030821  
 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,  
 CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,  
 GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,  
 LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL,  
 PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,  
 UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,  
 DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,  
 BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG  
 AU 2001086929 A5 20020313 AU 2001-86929 20010830  
 PRAI US 2000-654445 A 20000901  
 WO 2001-US27021 W 20010830

L9 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2003 ACS on STN  
 AN 2002:172150 CAPLUS  
 DN 136:227892  
 TI Analysis of protein binding interaction profiles using a nucleic acid  
**array** coupled to a solid silica support  
 IN Church, George; Bulyk, Martha; Choo, Yen  
 PA President and Fellows of Harvard College, USA; Gendaq, Ltd.  
 SO PCT Int. Appl., 97 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002018648	A2	20020307	WO 2001-US26435	20010824
	WO 2002018648	A3	20030109		
	W:		AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM		
	RW:		GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG		
	AU 2001085252	A5	20020313	AU 2001-85252	20010824
PRAI	US 2000-227900P	P	20000825		
	WO 2001-US26435	W	20010824		

L9 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2003 ACS on STN  
 AN 2002:143002 CAPLUS  
 DN 136:182443  
 TI Immobilized antibody **arrays**  
 IN Hu, Qianjin  
 PA USA  
 SO PCT Int. Appl., 17 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002014866	A2	20020221	WO 2001-US25450	20010813
	WO 2002014866	A3	20021010		
	W:		AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,		



LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT,  
 RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ,  
 VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,  
 DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,  
 BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU 2001084899 A5 20020225 AU 2001-84899 20010813  
 US 2002048823 A1 20020425 US 2001-929874 20010813  
 PRAI US 2000-224854P P 20000811  
 WO 2001-US25450 W 20010813

L9 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2003 ACS on STN  
 AN 2001:781183 CAPLUS  
 DN 135:328960  
 TI Library screening system to detect protein-protein interactions  
 IN Lilien, Jack; Elferink, Lisa A.; Balsamo, Janne; Kamholz, John  
 PA Wayne State University, USA  
 SO PCT Int. Appl., 59 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001079559	A1	20011025	WO 2001-US12457	20010418
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 2002081570	A1	20020627	US 2001-836865	20010418
PRAI US 2000-198122P	P	20000418		
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT				

L9 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2003 ACS on STN  
 AN 2000:909111 CAPLUS  
 DN 134:52245  
 TI Detection of nucleic acids in samples using ordered **arrays** of  
 probes by amplification of hybridization products  
 IN Lane, David J.; Farrell, Michael P.  
 PA Vysis, Inc., USA  
 SO U.S., 24 pp., Cont.-in-part of U.S. 5,837,466.  
 CODEN: USXXAM  
 DT Patent  
 LA English  
 FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6165714	A	20001226	US 1997-991675	19971216
US 5837466	A	19981117	US 1996-768177	19961216
JP 10293128	A2	19981104	JP 1997-346496	19971216
PRAI US 1996-768177	A2	19961216		
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT				

L9 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2003 ACS on STN  
 AN 2000:553286 CAPLUS

DN 133:145892  
TI Simultaneous measurement of gene expression and chromosomal abnormalities  
using nucleic acid microarrays  
IN Bao, Yijia; Che, Diping; Li, Wan-liang; Muller, Uwe Richard; Seelig,  
Steven A.; Shi, Jufang  
PA Vysis, Inc., USA  
SO Eur. Pat. Appl., 40 pp.  
CODEN: EPXXDW

DT Patent  
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 1026260	A1	20000809	EP 2000-300775	20000201
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	US 6251601	B1	20010626	US 1999-243067	19990202
	JP 2000232883	A2	20000829	JP 2000-25187	20000202
	US 2001018183	A1	20010830	US 2001-796230	20010228
PRAI	US 1999-243067	A	19990202		

RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L2 ANSWER 1 OF 3 MEDLINE on STN  
 AN 2001248185 MEDLINE  
 DN 21189419 PubMed ID: 11292345  
 TI Selection of ligands by **panning** of domain libraries displayed on phage lambda reveals new potential partners of synaptojanin 1.  
 AU Zucconi A; Dente L; Santonico E; Castagnoli L; Cesareni G  
 CS Department of Biology, University of Rome Tor Vergata, Rome, Via della Ricerca Scientifica, 00133, Italy.  
 SO JOURNAL OF MOLECULAR BIOLOGY, (2001 Apr 13) 307 (5) 1329-39.  
 Journal code: 2985088R. ISSN: 0022-2836.  
 CY England: United Kingdom  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 EM 200105  
 ED Entered STN: 20010517  
 Last Updated on STN: 20020420  
 Entered Medline: 20010510  
 AB One of the goals of functional genomics is the description of reliable and complete protein interaction networks. To facilitate ligand discovery from complex protein mixtures, we have developed an improved approach that is affected by a negligible fraction of false positives. We have combined a novel technique based on the display of cDNA libraries on the capsid of bacteriophage lambda and an efficient plaque assay to reveal phage displaying ligands that are enriched after only a couple of affinity purification steps. We show that the lambda display system has a unique ability to display, at high density, proteins ranging in size from a few to at least 300 amino acid residues. This characteristic permits attenuation of the size bias in the selection procedure and, at the same time, offers a sensitive plaque assay that permits us to do away with the ligand background without unduly increasing the number of selection cycles. By using a proline-rich fragment of the synaptojanin 1 protein as a bait, we have identified, in a brain cDNA display library, seven ligands all containing either SH3 or WW domains. Four of these correspond to proteins that have already been validated as physiological partners, while the remaining three are new partners, whose physiological relevance remains to be established. Two different proline-rich regions of the p21-activated protein kinase 1 (Pak1) and WAVE/SCAR2 protein retrieve from the library different proteins containing SH3 or WW domains.  
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 CT Check Tags: Comparative Study; Human; Support, Non-U.S. Gov't  
 Amino Acid Sequence  
**Bacteriophage T7: GE, genetics**  
 \*Bacteriophage lambda: GE, genetics  
 Binding Sites  
 Brain: ME, metabolism  
 Gene Library  
 Ligands  
 Microfilament Proteins: CH, chemistry  
 Microfilament Proteins: ME, metabolism  
 Molecular Sequence Data  
 Mutation: GE, genetics  
 \*Nerve Tissue Proteins: CH, chemistry  
 Nerve Tissue Proteins: GE, genetics  
 \*Nerve Tissue Proteins: ME, metabolism  
 Peptide Fragments  
 \*Peptide Library  
 \*Phosphoric Monoester Hydrolases: CH, chemistry  
 Phosphoric Monoester Hydrolases: GE, genetics  
 \*Phosphoric Monoester Hydrolases: ME, metabolism  
 Plaque Assay

Proline: ME, metabolism  
Protein Binding  
Protein Structure, Tertiary  
Protein-Serine-Threonine Kinases: CH, chemistry  
Protein-Serine-Threonine Kinases: ME, metabolism  
Recombinant Fusion Proteins: CH, chemistry  
Recombinant Fusion Proteins: ME, metabolism  
Substrate Specificity  
src Homology Domains

RN 147-85-3 (Proline)  
CN 0 (Ligands); 0 (Microfilament Proteins); 0 (Nerve Tissue Proteins); 0  
(Peptide Fragments); 0 (Peptide Library); 0 (Recombinant Fusion Proteins);  
0 (WAVE protein); EC 2.7.1.- (p21-activated kinase 1); EC 2.7.1.37  
(Protein-Serine-Threonine Kinases); EC 3.1.3 (Phosphoric Monoester  
Hydrolases); EC 3.1.3.- (synaptojanin)

## METHOD TO IDENTIFY GENE FUNCTION USING SMALL MOLECULE PROBES

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Inventor(s): MCKENZIE KATHLEEN M; SCHE PAUL P; AUSTIN DAVID J; SAVINOV SERGEY N  
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EC Classification: C12N15/10C1, G01N33/543  
Equivalents: AU7343700, CA2383186, ☐ EP1212453 (WO0118234), JP2003508078T  
Cited Documents:

### Abstract

Methods for identifying genes which bind to natural products and other small molecules using a phage display system are described. Phage displaying protein which binds the target molecule are selected by affinity chromatography using a solid support to which a small molecule non-peptide bait is coupled. The selectively bound phage can then be amplified and the DNA inserts encoding the binding protein sequenced. The specifically bound protein is then useful to screen for therapeutic candidates which can then be used to treat conditions modulated by the target protein.

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**Regular Article****Selection of Ligands by Panning of Domain Libraries Displayed on Phage Lambda Reveals New Potential Partners of Synaptojanin 1<sup>\*1</sup>, <sup>\*2</sup>****Adriana Zucconi<sup>a</sup>, Luciana Dente<sup>a</sup>, Elena Santonico<sup>a</sup>, Luisa Castagnoli<sup>a</sup> and Gianni Cesareni<sup>a, f1, f2</sup>**<sup>a</sup> Department of Biology, University of Rome Tor Vergata, Via della Ricerca Scientifica, 00133, Rome, Italy

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**Abstract**

One of the goals of functional genomics is the description of reliable and complete protein interaction networks. To facilitate ligand discovery from complex protein mixtures, we have developed an improved approach that is affected by a negligible fraction of false positives. We have combined a novel technique based on the display of cDNA libraries on the capsid of bacteriophage lambda and an efficient plaque assay to reveal phage displaying ligands that are enriched after only a couple of affinity purification steps. We show that the lambda display system has a unique ability to display, at high density, proteins ranging in size from a few to at least 300 amino acid residues. This characteristic permits attenuation of the size bias in the selection procedure and, at the same time, offers a sensitive plaque assay that permits us to do away with the ligand background without unduly increasing the number of selection cycles. By using a proline-rich fragment of the synaptojanin 1 protein as a bait, we have identified, in a brain cDNA display library, seven ligands all containing either SH3 or WW domains. Four of these correspond to proteins that have already been validated as physiological partners, while the remaining three are new partners, whose physiological relevance remains to be established. Two different proline-rich regions of the p21-activated protein kinase 1 (Pak1) and WAVE/SCAR2 protein retrieve from the library different proteins containing SH3 or WW

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domains.

**Author Keywords:** phage display; cDNA library; SH3; WW; protein interaction

\*1 Abbreviations used: PRD, proline-rich domain; GST, glutathione *S*-transferase; Syn, synaptojanin; FBP, formin-binding protein; BSA, bovine serum albumin

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